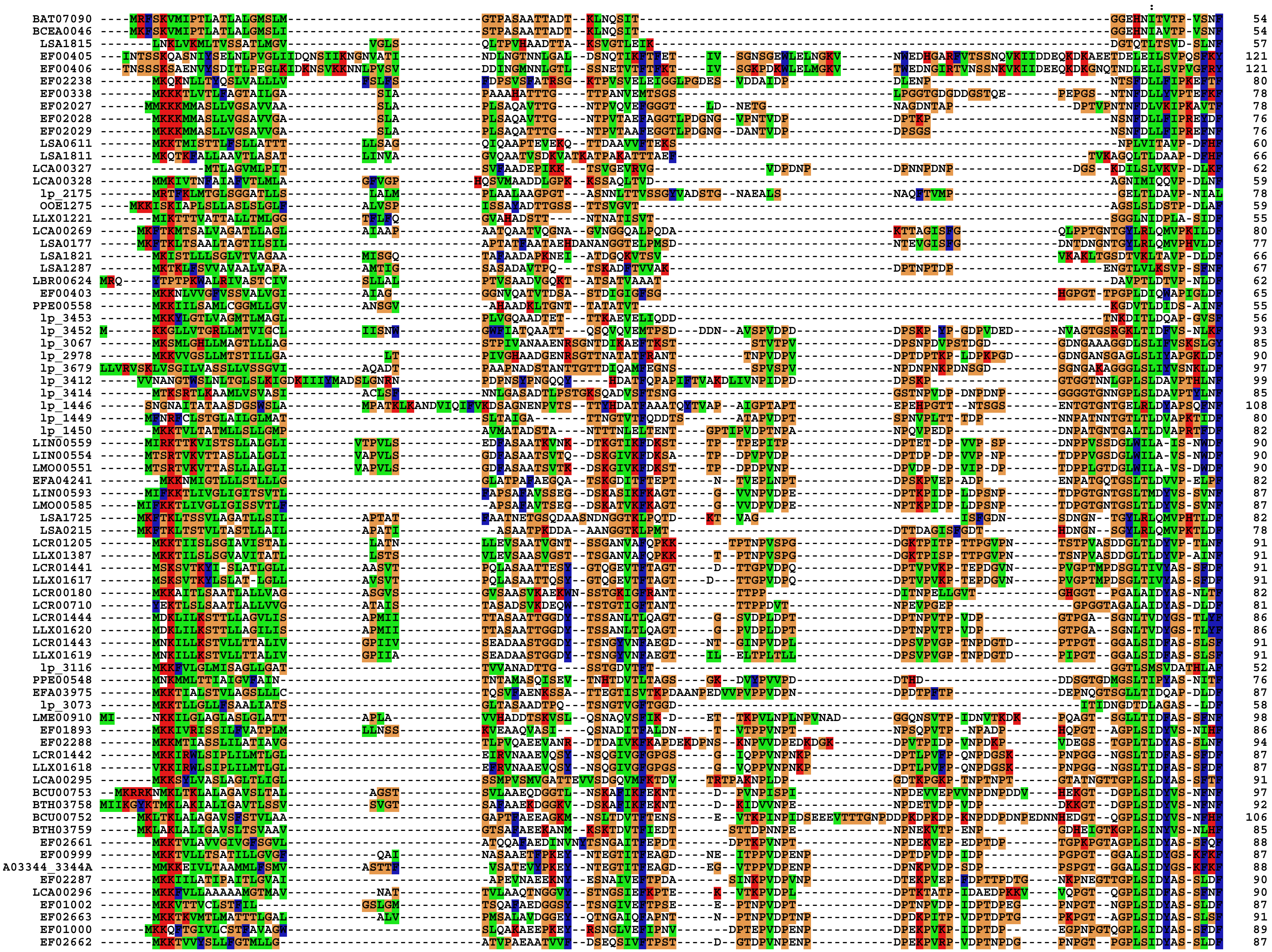

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    BCEA0046 ----MKFSKVMIPTLATLALGMSLI--------------------------STPASAATTADT--KLNQSIT---------------------------------------------------------------GGEHNIAVTP-VSNF   54
     LSA1815 -------LNKLVKMLTVSSATLMGV-----------VGLS-----------QLTPVHAADTTA--KSVGTLEIK-------------------------------------------------------------DGTQTLTSVD-SLNF   57
     EF00405 ---INTSSKQASNIYSELNLPVGLIIDQNSIIKNGNVATI-----------NDLNGTNNLGAL--DSNQTIKFTFET----IV--SGNSGEWLELNGKV-------NWEDHGARFVTSSNQVKIIDDEQKDKAEETDELEILSVPQSFKY  121
     EF00406 ---TNSSSKSAENVYSDITLPEGLKIDKNSVKKNNLPVSV-----------DDINGMNNLGTL--SSNETVTFTFKT----IV--SGKPDKWLELMGKV-------TWEDNGIRTVNSSNKVKIIDEEQKDKGNQTNDLELLSVPVGFRY  121
     EF02238 -------MKQKNLLTYQSLVALLLV----------FSLFS-----------FDPSVSFATRSG--KTPVSVELEIGGLPGDES--VDDAIDP--------------DLENP------------------------NTSFDLLFIPKEFTF   80
     EF00338 -------MKKKTLVTLFAGTAILGA------------SIA-----------PAAAHATTTG----TTPANVEMTSGS-----------------------------LPGGTGDGDDGSTQE-------PEPGS--NTNFDLLYVPTEFKF   78
     EF02027 ------MMKKKMMASLLVGSAVVAA------------SLA-----------PLSAQAVTTG----NTPVQVEFGGGT----LD--NETG-----------------NAGDNTAP----------------DPTVPNTNFDLVKIPKAVTF   78
     EF02028 -------MKKKMMASLLVGSAVVGA------------SLA-----------PLSAQAVTTG----NTPVTAEFAGGTLPDGNG--VPNTVDP--------------DPTKP------------------------NSNFDLLFIPREYDF   76
     EF02029 -------MKKKMMASLLVGSAVVGA------------SLA-----------PLSAQATTTG----NTPVTAAFEGGTLPDGNG--DANTVDP--------------DPSGS------------------------NSNFDLLFIPREFNF   76
     LSA0611 -------MKKTMISTTLFSLLATTT----------LLSAG-----------QIQAAPTEVEKQ--TTDAAVVFTEKS-----------------------------------------------------------NPLVITAVP-DFHF   60
     LSA1811 -------MKQTKFALLAAVTLASAT----------LINVA-----------GVQAATVSDKVATKATPAKATTTAEF-------------------------------------------------------TVKAGQLTLDAAP-DFHF   66
    LCA00327 --------------MTLAGVMLPIT--------------------------SVFAADEPIKK---TSVGEVRVG---------------VDPDNP-----------DPNNPDNP----------------DGS--KDILSLVKVP-DLKF   62
    LCA00328 -------MMKIVTNFAIAFVTLMLA----------GFVGP----------HQSVMAADDLGPK--KSSAQLTVD-------------------------------------------------------------AGNIMIQQVP-DLNF   59
     lp_2175 -------MRTFKLMTGLSGGATLLS-----------LALM-----------PLAALAAGPGT---ASNNLTTVSSGYVADSTG--NAEALS---------------NAQFTVMP----------------------GELTLDAVP-NIAL   78
     OOE1275 ----MKKISKIAPLSLLASLSLGLF----------ALVSP-----------ISSAYADTTGSS--TTSVGVT---------------------------------------------------------------AGSLSLDSTP-DLAF   59
    LLX01221 -------MIKTTTVATTALLTMLGG----------TFLFQ-----------GVAHADSTT-----NTNATISVT-------------------------------------------------------------SGGLNIDPLA-SIDF   55
    LCA00269 -----MKFTKMTSALVAGATLLAGL----------AIAAP-----------AATQAATVQGNA--GVNGGQALPQDA-----------------------------KTTAGISFG-------------QLPPTGNTGYLRLQMVPKILDF   80
     LSA0177 -----MKFTKLTSAALTAGTILSIL--------------------------APTATFAATAEHDANANGGTELPMSD-----------------------------NTEVGISFG-------------DNTDNGNTGYLRLQMVPHVLDF   77
     LSA1821 -------MKISTLLLSGLVTVAGAA----------MISGQ-----------TAFAADAPKNEI--ATDGQKVTSV-----------------------------------------------------VKAKLTGSDTVKLTAVP-DLDF   66
     LSA1287 -------MKTKLFSVVAVAALVAPA----------AMTIG-----------SASADAVTPQ----TSKADFTVVAK------------------------------DPTNPTDP--------------------ENGTLVLKSVP-SFNF   67
    LBR00624 MRQ----YTPTPKWALRIVASTCIV----------SLLAL-----------PTVSAADVGQKT--ATSATVAAAT------------------------------------------------------------DAVPTLDTVP-NLDF   62
     EF00403 -------MKKNLVVGFVSSVALVGI----------AIAG------------GGNVQATVTDSA--STDIGIGFSG-----------------------------------------------------HGPGT-TPGPLDIQWAPIGLDF   65
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     lp_3453 -------MKKYLGTLVAGMTLMAGL--------------------------PLVGQAADTET---TTKAEVELIQDD---------------------------------------------------------TNKDITLDQAP-GVSF   56
     lp_3452 M------KKGLLVTGRLLMTVIGCL----------IISNW-----------GWFIATQAATT---QSQVQVEMTPSD---DDN--AVSPVDPD-------------DPSKP-YP-GDPVDED------NVAGTGSRGKLTIDFVS-NLKF   93
     lp_3067 -------MKSMLGHLLMAGTLLLAG--------------------------STPIVANAAENRSGNTDIKAEFTKST----------STVTPV-------------DPSNPDVPSTDGD---------GDNGAAAGGDLSLIFVSKSLGY   85
     lp_2978 -------MKKVVGSLLMTSTILLGA-------------LT-----------PIVGHAADGENRSGTTNATATFRANT---------TNPVDPV-------------DPTDPTKP-LDPKPGD------GDNGANSGAGLSLIYAPGKLDF   90
     lp_3679 LLVRVSKLVSGILVASSLLVSSGVI----------AQADT-----------PAAPNADSTANTTGTTDIQAMFEGNS----------SPVSPV-------------NPDNPNKPDNSGD---------SGNGAKAGGGLSLIYVSNKLDF   97
     lp_3412 -----VVNANGTWSLNLTGLSLKIGDKIIIYMADSLGNRN-----------PDPNSYPNGQQY-----HDATFQPAPIFTVAKDLIVNPIDPD-------------DPSKP-----------------GTGGTNNLGPLSLDAVPTHLNF   99
     lp_3414 -------MTKSRTLKAAMLVSVASI----------ACLSF-----------NNLGASADTLPSTGKSQADVSFTSNG-----------------------------GSTNPVDP-DNPDNP-------GGGGTGNNGPLSLDAVPTYLNF   85
     lp_1446 ------SNGNAITATAASDGSWSLA----------MPATKLKANDVIQIFVKDSAGNENPVTS--TTYHDATFAAATQYTVAP--AIGPTAPT-------------EPEHPGTT--NTSGS-------ENTGTGNTGELRLDYAPSQFNF  108
     lp_1449 ------MFNRFCLSTGLAILGLMAT--------------------------SLTAIGA-------TTNGTVTFQDDTS-------ATAPVDPT-------------SPNVPLTT-TDP----------NNPATNNTGTLTLDVAPKTIDF   80
     lp_1450 -------MKKTVLTATMLLSLLGMP--------------------------AVMATADSTA----NTTTNLELTENT----GPTIPVDPTNPA-------------NPQVPEDP--------------DNPATGNTGALTLDVAPRTFDF   82
    LIN00559 ------MIRKTTKVISTSLLALGLI---------VTPVLS-----------EDFASAATKVNK--DTKGTIKFDKST----TP--TPEPITP--------------DPTET-DP-VVP-SP-------DNPPVSSDGLWILA-IS-NWDF   90
    LIN00554 ------MTSRTVKVTTASLLALGLI---------VAPVLS-----------GDFASAATSVTQ--DSKGIVKFDKSA----TP--DPVPVDP--------------DPTDP-DP-VVP-NP-------TDPPVGSDGLWILA-VS-NWDF   90
    LMO00551 ------MTSRTVKVTTASLLALGLI---------VAPVLS-----------GDFASAATSVTK--DSKGIVKFDKST----TP--DPDPVNP--------------DPVDP-DP-VIP-DP-------TDPPLGTDGLWILA-VS-DWDF   90
    EFA04241 --------MKKNMIGTLLLSTLLLG--------------------------GLATPAFAEGQA--TSKGDITFTEPT-----N--TVEPLNPT-------------DPSKPVEP-ADP----------ENPATGQTGSLTLDVVP-ELPF   82
    LIN00593 ------MIFKKTLIVGLIGITSVTL--------------------------FAPSAFAVSSEG--DSKASIKFKAGT-----G--VVNPVDPE-------------DPTKPIDP-LDPSNP-------TDPGTGNTGSLTMDYVS-SVNF   87
    LMO00585 -----MIFKKTLIVGLIGISSVTLF---------------------------APSAFAVTSEG--DSKATVKFKAGT-----G--VVDPVDPE-------------NPTKPIDP-LDPSNP-------TDPGTGNTGSLTLDYVS-SVNF   87
     LSA1725 -----MKFTKLTSSVLAGATLLSIL----------APTAT-----------FAATNETGSQDAASNDNGGTKLPQTD----KT--VAG---------------------------ISFGDN-------SDNGN--TGYLRLQMVPHTLDF   82
     LSA0215 -----MKFTKLTSTVLTASTLLAIL----------APATI-------------ASAATPKDDA--AANGGTKLPMT------------------------------DTTDAGISFGDT----------HDNGN--SGYLRLQMVPKTLDF   78
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    LLX01387 -------MKKTILSLSGVAVITATL-----------LSTS-----------VLEVSAASVGST--TSGANVAFQPKK-----T--PTNPVSPG-------------DGKTPISP-TTPGVPN------TSNPVASDDGLTLDYVP-AINF   91
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    PPE00548 -------MNKMMLTTIAIGVFAIN---------------------------TNTAMASQISEV--TNHTDVTLTAGS----GK--DVYPVVPD-------------DTHD------------------DDSGTGDMGSLTIPYAS-NITF   76
    EFA03975 -------MKKTIALSTVLAGSLLLC--------------------------TQSVFAENKSSA--TTEGTISVTKPDAANPEDVVPVPPVDPN-------------DPDTPFTP--------------DEPNQGTSGLLTIDQAP-DLDF   87
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    LME00910 MI-----NKKILGLAGLASLGLATT----------APLA------------VVHADDTSKVSL--QSNAQVSFIK-D----ET--TKPVLNPLNPVNAD-------GGQNSVTP-IDNVTKDK-----PQAGT--SGLLTIDFAS-SFNF   98
     EF01893 -------MKKIVRISSILFVATPLM----------LLNSS-----------KVEAAQVASI----QSNADITFALDN-----T--VTPPVNPT-------------NPSQPVTP--NPADP-------HQPGT--AGPLSIDYVS-NIHF   86
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    BTH03758 MIIKGYKTMKLAKIALIGAVTLSSV-----------SVGT-----------SAFAAEKDGGKV--DSKAFIKFEKNT-----D--KIDVVNPE-------------NPDETVDP-VDP----------DKKGT--DGPLSIDYVS-NFNF   92
    BCU00752 -----MKLTKLALAGAVSFSTVLAA--------------------------GAPTFAEEAGKM--NSLTDVTFTENS-----E--VTKPINPIDSEEEVTTTGNPDDPKDPKDP-KNPDDPDNPEDNNHEDGT--QGPLSIDYVS-NFHF  106
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     EF00999 -------MKKTVLLTSATILLGVGF------------QAI-----------NASAAETFPKEY--NTEGTITFEAGD----NE--ITPPVDPENP-----------DPTDPVDP-IDP----------PGPGT--GGALSIDYGS-KFKF   87
A03344_3344A -------MMKKEIVLTAAMMLFSMV----------ASTTF------------VSATEVYPKEY--NTEGTITFEAGD----EG--VTPPVDPENP-----------DPNKPVDP-SDP----------PSPGT--GGALSIDYGS-KFKF   88
     EF02287 -------MKKIILATIPAITLGVAI---------------------------APEVNAEEKNY--ESNAIVEFTPDA-------SINKPVDPVNP-----------DTEKPVEP-FDPTTPDTG----NKPNEGTTGPLSIDYAS-SLDF   90
    LCA00296 -------MKKFVLLAAAAAMGTMAV------------NAT-----------TVLAAQTNGGVY--STNGSIEFKPTE-----K--VTKPVDPL-------------DPTKTATP-IDAEDPKKV----VQPGT--QGPLSIDFAS-SFNF   90
     EF01002 -------MKKVTTVCLSTFIL--------------GSLGM-----------TSQAFAEDGGSY--TSNGIVEFTPSE-----E--PTNPVDPT-------------DPTNPVDP-IDPTDPEG-----PNPGT--NGPLSIDYAS-SLDF   87
     EF02663 -------MKKTKVMTLMATTTLGAL------------ALV-----------PMSALAVDGGEY--QTNGAIQFAPNT-----N--PTNPVDPTNP-----------DPDKPITP-VDPTDPTG-----PKPGT--AGPLSIDYAS-SLSF   91
     EF01000 ------MKKQFTGIVLCSTFAVAGW--------------------------SLQAKAEEPKEY--RSNGLVEFIPNV-------DPTEPVDPENP-----------DPEKPVKP-IDPTDP-------EGPNPGTQGPLSIDYAS-SFDF   89
     EF02662 -------MKKTVVYSLLFGTMLLG---------------------------ATVPAEAATVVF--DSEQSIVFTPST-----D--GTDPVNPENP-----------DPEKPVRP-VDPTNPDG-----PNPGT--PGPLSIDYAS-SLDF   87
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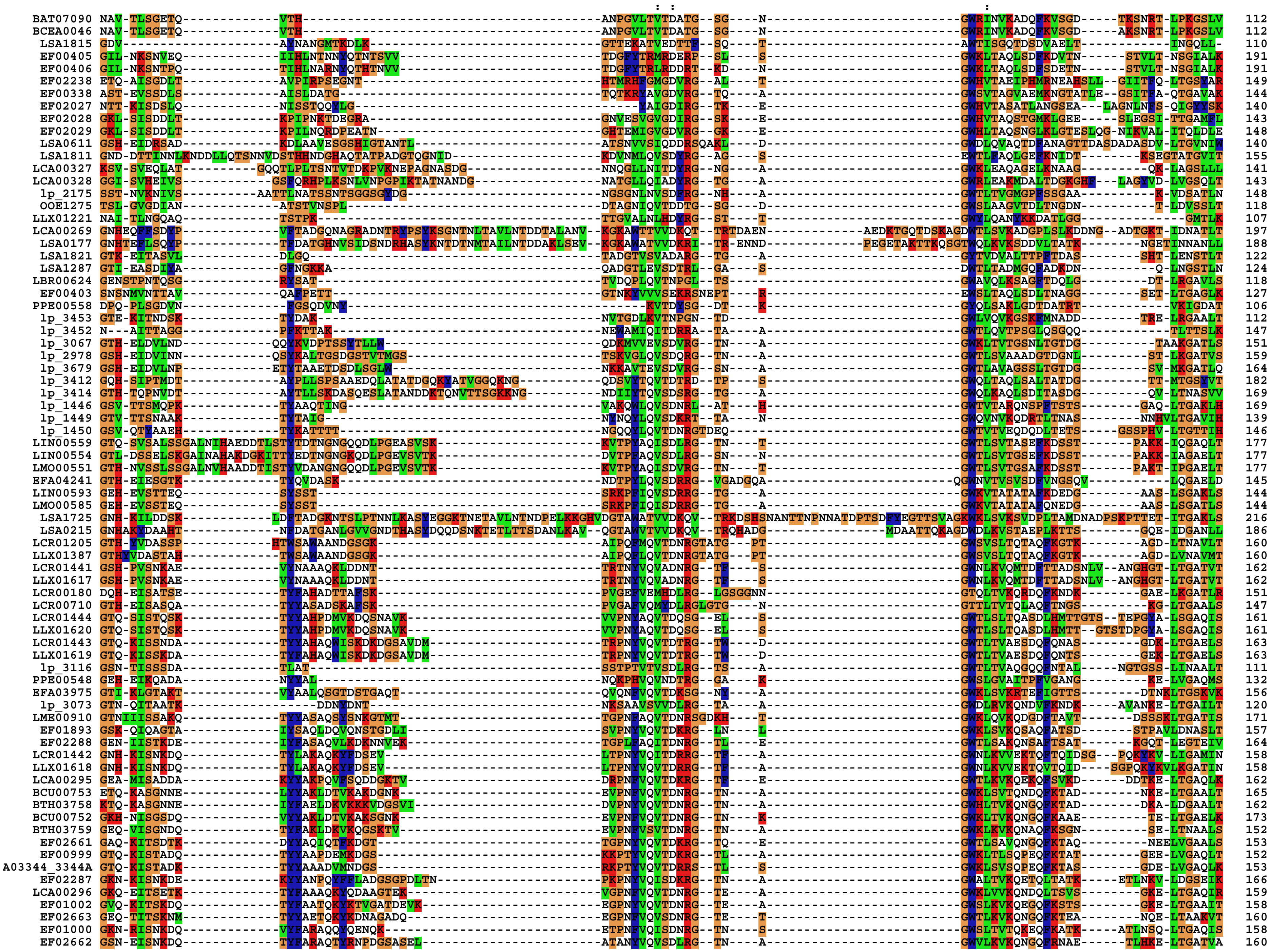

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    BCEA0046 NAV-TLSGETQ-------------VTH----------------------------------------ANPGVLTVTDATG--SG----N--------------------------GWRINVKADQFKVSGD-----AKSNRT-LPKGSLV   112
     LSA1815 GDV---------------------AYNANGMTKDLK-------------------------------GTTEKATVEDTTF--SQ----T--------------------------AWTISGQTDSDVAELT------------INGQLL-   110
     EF00405 GIL-NKSNVEQ-------------IIHLNTNNYQTNTSVV---------------------------TDGFYTRMRDERP--SL----S--------------------------GWKLTAQLSDFKDVTN------STVLT-NSGIALK   191
     EF00406 GIL-NKSNTPQ-------------TIHLNARNYQTHTNVV---------------------------TDGFYTRLRDDRT--KD----N--------------------------GWKLTAQLSDFSDETN------STVLT-NSGIALK   191
     EF02238 ETQ-AISGDLT-------------AVPIRPSEGNT--------------------------------HTMRHFGMGDVRG--AL----T--------------------------GWHVTAEIPHMRNEAHSLL--GIITFQ-LTGSYAR   149
     EF00338 AST-EVSSDLS-------------AISLDATG-----------------------------------TQTKRYAVGDVRG--TQ----A--------------------------GWSVTAGVAEMKNGTATLE--GSITFA-QTGAVAK   144
     EF02027 NTT-KISDSLQ-------------NISSTQQYLG--------------------------------------YAIGDIRG--TK----E--------------------------GWHVTASATLANGSEA---LAGNLNFS-QIGYYSK   140
     EF02028 GKL-SISDDLT-------------KPIPNKTDEGRA-------------------------------GNVESVGVGDIRG--SK----E--------------------------GWHVTAQSTGMKLGEE-----SLEGSI-TTGAMFL   143
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     LSA1811 GND-DTTINNLKNDDLLQTSNNVDSTHHNDGHAQTATPADGTQGNID--------------------KDVNMLQVSDYRG--AG----S--------------------------EWTLFAQLGEFKNIDT--------KSEGTATGVIT   155
    LCA00327 KSV-SVEQLAT----------GQQTLPLTSNTVTDKPVKNEPAGNASDG------------------NNQGLLNITDYRG--NG----A--------------------------GWKLEAQAGELKNAAG---------QK-LAGSLLL   141
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     OOE1275 TSL-GVGDIAN-------------ATSTVNSPL----------------------------------DTAGNIQVTDDTG--SG----D--------------------------GWSLAAGVTDLTNGDN----------T-LDVSSLT   118
    LLX01221 NAI-TLNGQAQ-------------TSTPK--------------------------------------TTGVALNLHDYRG--ST----T--------------------------GWYLQANYKKDATLGG--------------GMTLK   107
    LCA00269 GNHEQFFSDYP-------------VFTADGQNAGRADNTRYPSYKSGNTNLTAVLNTDDTALANV--KGKAWTTVVDKQT--TRTDAEN-------------AEDKTGQTDSKAGDWTLSVKADGPLSLKDDNG--ADTGKT-IDNATLT   197
     LSA0177 GNHTEFLSQYP-------------TFDATGHNVSIDSNDRHASYKNTDTNMTAILNTDDAKLSEV--KGKAWATVVDKRI--TR-ENND-------------PEGETAKTTKQSGTWQLKVKSDDVLTATK--------NGETINNANLL   188
     LSA1821 GTK-EITASVL-------------DLGQ---------------------------------------TADGTVSVADARG--TG----A--------------------------GYTVDVALTTPFTDAS--------SHT-LENSTLT   122
     LSA1287 GTI-EASDIYA-------------GFNGKKA------------------------------------QADGTLEVSDTRL--GA----S--------------------------DWTLTADMGQFADKDN----------Q-LNGSTLN   124
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     EF00403 SNSNMVNTTAV-------------QAFPETT------------------------------------GTNKYVVVSEKRSNEPT----R--------------------------EWSLTAQLSDLTNAGG--------SET-LTGAGLK   127
    PPE00558 DPQ-PLSGDVN--------------FGSQDVNY----------------------------------      KVTDYSG--DT----K--------------------------GYQLSAKLGDTDATRT------------VKIGDAT   106
     lp_3453 GTE-KITNDSK-------------TYDAK--------------------------------------NVTGDLKVTNPGN--TD     --------------------------GWLVQVKGSKFMNADD--------TRE-LRGAALT   112
     lp_3452 N---AITTAGG-------------PFKTTAK------------------------------------NEWAMIQITDRRA--TA----A--------------------------GWTLQVTPSGLQSGQQ------------TLTTSLK   147
     lp_3067 GTH-ELDVLND------------QQYKVDPTSSYTLLW-----------------------------QDKMVVEVSDVRG--TN----A--------------------------GWKLTVTGSNLTGTDG----------TAAKGATLS   151
     lp_2978 GSH-EIDVINN------------QSYKALTGSDGSTVTMGS--------------------------TSKVGLQVSDQRG--TN----A--------------------------GWTLSVAAADGTDGNL---------ST-LKGATVS   159
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     lp_3412 GQH-SIPTMDT-------------AYPLLSPSAAEDQLATATDGQKYATVGGQKNG-----------QDSVYTQVTDTRD--TP----S--------------------------GWQLTAQLSALTATDG---------TT-MTGSYVT   182
     lp_3414 GTH-TQPNVDT-------------AYTLLSKDASQESLATANDDKTQNVTTSGKKNG----------NDIIYTQVSDSRG--TG----A--------------------------GWQLKAQLSDITASDG---------QV-LTNASVV   169
     lp_1446 GSV-TTSMQPK-------------TYAAQTING----------------------------------VAKQWLQVSDNRL--AT----H--------------------------GWTVTARQNSPFTSTS--------GAQ-LTGAKLH   169
     lp_1449 GTV-TTSNAAK-------------TYTAIG-------------------------------------NYNQYLQVSDKRT--TA----N--------------------------GWQVNVKQDRTLTNAS--------NNHVLTGAVIH   139
     lp_1450 GSV-QTYAAEH-------------TYKATTTT-----------------------------------NGQQYLQVTDNRGTDEQ     --------------------------GWTVTVEQDQDLTETS-----GSSPHV-LTGTTIH   146
    LIN00559 GTQ-SVSALSSGALNIHAEDDTLSTYTDTNGNGQQDLPGEASVSK----------------------KVTPYAQISDLRG--TN----T--------------------------GWTLSVTASEFKDSST-------PAKK-IQGAQLT   177
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     LSA0215 GNHAKYDAAHT-------------NFDATGANLGVVGNDTHASYDQQDSNKTETLTTSDANLKAV--QGTAWVTVVDKQV--TRQHADG----------------MDAATTQKAGDWDLKVSTAEPLKTTS--------GQE-IDGANLL   186
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    EFA03975 GTI-KLGTAKT-------------VYAALQSGTDSTGAQT---------------------------QVQNFVQVTDKSG--NY----A--------------------------GWKLSVKRTEFIGTTS--------DTNKLTGSKVK   156
     lp_3073 GTN-QITAATK-------------     DDNYDNT-------------------------------NKSAAVSVVDLRG--TA----A--------------------------GWDLRVKQNDVFKNDK-----AVANKE-LTGAILT   120
    LME00910 GTNIIISSAKQ-------------TYYASAQSYSNKGTMT---------------------------TGPNFAQVTDNRSGDKH----T--------------------------GWKLQVKQDGDFTAVT-------DSSSKLTGATIS   171
     EF01893 GSK-QIQAGTA-------------IYSAQLDQVQNSTGDLI--------------------------SVPNYVQVTDKRG--LN----L--------------------------GWKLSVKQSAQFATSD-------STPAVLDNASLT   157
     EF02288 GEN-IISTKDE-------------IYFASAQVLKDKNNVEK--------------------------TGPLFAQITDNRG--TL----E--------------------------GWTLSAKQNSAFTSAT-------KGQT-LEGTEIV   164
    LCR01442 GNH-KISNKDQ-------------TYLAKAQKYFDSEV-----------------------------LTPNYVQITDRRG--TF----A--------------------------GWNLKVVEKTQFTQIDSG---PQKYKV-LIGAMIN   158
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    LCA00295 GEA-MISADDA-------------KYYAKPQVFSQDDGKTV--------------------------DRPNFVQVTDKRG--TF----E--------------------------GWTLKVKQEKQFSVKD------DDTKE-LTGAQLK   162
    BCU00753 ETQ-KASGNNE-------------LYYAKLDTVKAKDGNK---------------------------EVPNFVQVTDNRG--TN----A--------------------------GWKLSVTQNDQFKTAD--------NKE-LTGAALT   165
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     EF01000 GKN-RISNKDQ-------------VYFARAQQYQENQK-----------------------------ETPNFVQISDNRG--TN----S--------------------------GWSLTVTQKEQFKATK-----ATLNSQ-LTGAQIS   158
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     EF02028 YPLIYNEETKTYDY--QSAD---------------LADPVTKP-----------------------ETVDTTAFSIA-------LGGDA-VLLANAT-----------AGKGQGLWQFSF-------------------------RPYLN  209
     EF02029 YEATSNSYVALTTA--VSTP---------------EVRP---------------------------QLAAPQNWTLD-------LGGEA-QLMANAA-----------AGQGQGLWQFS------------------------LFNTALN  211
     LSA0611 FKTPNV-------T--IDGA---------------NKGDA--------------------------ALPTTSDQTVQ-------VNDQA--STFMKG-----------GATSFGSVAATLGTAPTSG----------------TDSDAIF  204
     LSA1811 IGKGVD----------NLTN----------------------------------------------TTIGKDAQVIM----------NTAKTLKNTP-----------EKLGAQTTTADFSA---------------------PGDKASS  207
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    LCA00328 ASNPDI------------NP---------------INPAG--------------------------SNVPRLNFAKD-------NTSVSSTVVWQAD-----AETGTKSGQGQGNNQTTI-----------------------GTRTALT  205
     lp_2175 LNMTKG------NA--DNAN---------------TAAPT--------------------------ALSLNQSEVTN-------GWVASPQTLWNAA-----------ADSGEGSNTA-------------------------TTATSSS  206
     OOE1275 INNVSI-----------------------------------TPS------------------------------------------TDGSTTSTVWDNS-----------ASTGGTLTQA-------------------------LSSSNTS  157
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     LSA1287 LASTGS----------LGED---------------------------------------------------LATAIK-------DDASA-VEVVKGN-----------GAHGVDTFNMA------------------------AADSKLT  170
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     lp_3452 LGAVQL-----RPG--AGNV---------------STAPN-----------------------------VVNTGELV-------AGLAN--NVVIAP-----------PNTGLGTWLVVLN----------------------RGQVPTE  204
     lp_3067 LPKGDV----------VNSG---------------SEANG--------------------------AVATASEVALN-------GTVGS-SAVLNAD-----------KGGGSGVTVS-------------------------RDPKALT  206
     lp_2978 LPAGTVISSGSEASNGSTGG---------------NGAVGQAVELDL-------------------GSQASTSAGAS-------FTGTTSGNVMTAA-----------DKSGAGITSDL------------------------LDPAAVK  233
     lp_3679 LPKGTV----------TNSG---------------ATNN---------------------------GVQSTEALNVL-------DGNSA--TVLSAA-----------KDHGAGVTVDQ------------------------IDPSNVK  218
     lp_3412 LTSGTAQYLNASTSKWVTAT---------------DQN----------------------------QATLPAVIKLT-------PGATQQTLIAGTT-----------SQQGVGTNQQI------------------------WNVNNVA  247
     lp_3414 LSGGTPQYLTGEANQQSWVT---------------AADAN--------------------------QATVATPIVLN-------AGASSTTDVATAT-----AGSKVGDGQGMGVNQQY------------------------WNINNVQ  242
     lp_1446 IPAGQT----------YNER----------------------------------------------ATGQLKSYAVD-------LTTAE-QPVFAAP-----------ATANVGKDLSTNV----------------------WQPTQVQ  222
     lp_1449 LPQGTA-----RNS--LNEP---------------ASVA---------------------------DSNLVVAPSVS-------VTTAD-QVVFSAP-----------NRAGVGKATSTNT----------------------WNAGAVT  199
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    LIN00554 IPKSTV------KS--KDST---------------AKAP---------------------------TGYDNVAISMT-------GGAAV--PVMAAKDLQATTPTDFSDDEGMGTWTDSFGSAEVSA----------------TETSKPK  252
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    LLX01387 FNNDKT-----NTV--VSTS---------------MNKAS--------------------------STVNTATNALV-------PGTAV--NIFQAD-----------AGTGTGTNLLSFGAGDGSTLVTDPETLDSATNTTGKVDPNIT  242
    LCR01441 LGDAEI----------QGAG---------------TANP---------------------------ADISSAITVLT-------PGVQS-TTILGAT-----------AGHGSGNSLLDFGGKDGA-----------------KKDTAIK  224
    LLX01617 LGDAEI----------QGAG---------------TANP---------------------------ADISSATTVLT-------PGVQS-ATILGAT-----------AGHGSGNSLLDFGGKDGS-----------------TKDTAIK  224
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    LCR00710 FSSGAG-----VNA--DASG---------------SYVPK-----------------------------STASYTLT-------PGTAQ--EVMS-------------TDGTVGQYLTSYGKAADYQGN--------------EAGGPIS  210
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    BCU00752 LSNPFV------NS--ATDK---------------KFSPT------------------------------AKEVTLN-------PDGST-QEVTIAE-----------AGNGMGTWTTAYGKDNV------------------EGAKSVG  233
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     EF02662 FTEPSV----------RSNA---------------TDVL---------------------------PPTATANIQLD-------AAGAE-TVVMQAP-----------EKTGAGTWITLWGQAEKVTEKNQQGQQVNA-----TITRAIS  234
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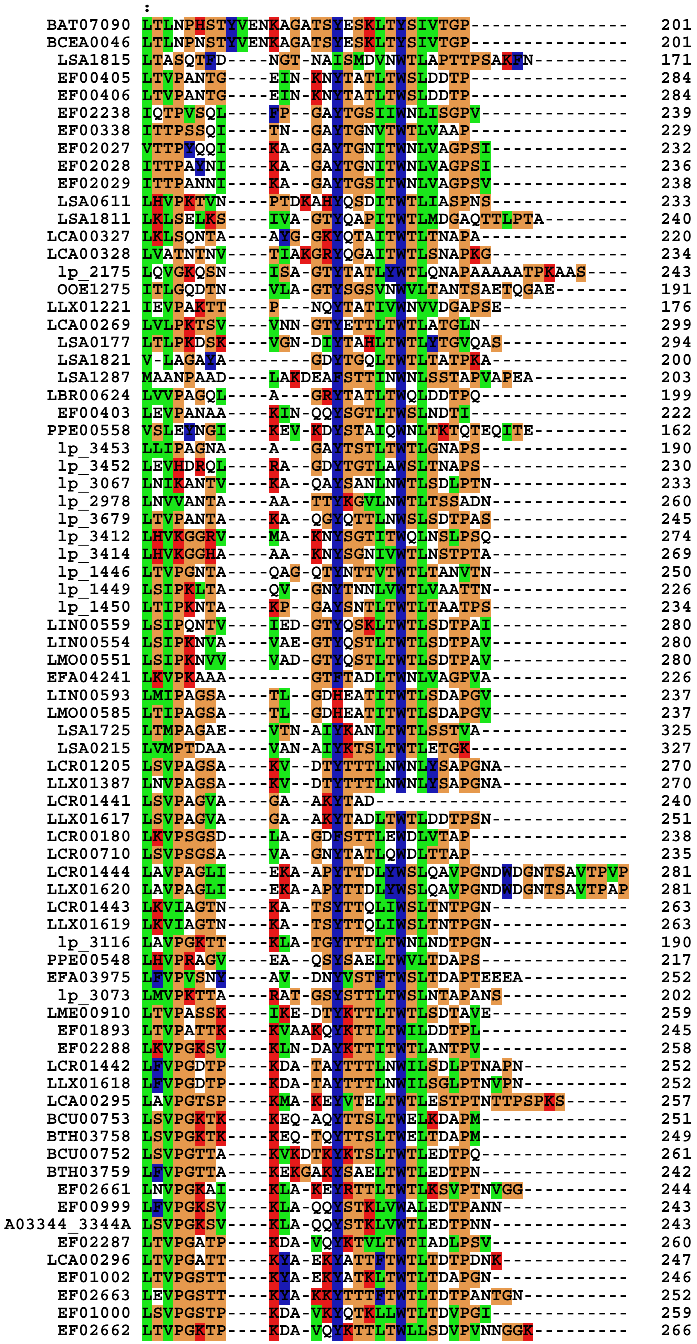

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    LLX01221 IEVPAKTT----P---NQYTATIVWNVVDGAPSE------------   176
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     lp_3412 LHVKGGRV----MA--KNYSGTITWQLNSLPSQ-------------   274
     lp_3414 LHVKGGHA----AA--KNYSGNIVWTLNSTPTA-------------   269
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     lp_1449 LSIPKLTA----QV--GNYTNNLVWTLVAATTN-------------   226
     lp_1450 LTIPKNTA----KP--GAYSNTLTWTLTAATPS-------------   234
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    LIN00554 LSIPKNVA----VAE-GTYQSTLTWTLSDTPAV-------------   280
    LMO00551 LSIPKNVV----VAD-GTYQSTLTWTLSDTPAV-------------   280
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     LSA0215 LVMPTDAA----VAN-AIYKTSLTWTLETGK---------------   327
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    LCR01441 LSVPAGVA----GA--AKYTAD------------------------   240
    LLX01617 LSVPAGVA----GA--AKYTADLTWTLDDTPSN-------------   251
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    LCR00710 LSVPSGSA----VA--GNYTATLQWDLTTAP---------------   235
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    LCR01443 LKVIAGTN----KA--TSYTTQLIWSLTNTPGN-------------   263
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    PPE00548 LHVPRAGV----EA--QSYSAELTWVLTDAPS--------------   217
    EFA03975 LFVPVSNY----AV--DNYVSTFTWSLTDAPTEEEA----------   252
     lp_3073 LMVPKTTA----RAT-GSYSTTLTWSLNTAPANS------------   202
    LME00910 LTVPASSK----IKE-DTYKTTLTWTLSDTAVE-------------   259
     EF01893 LTVPATTK----KVAAKQYKTTLTWILDDTPL--------------   245
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Figure 5:

Multiple sequence alignment of CscB proteins. Proteins IDs can be found in additional file Table 5. Colour coding of highly conserved residues: green, hydrophobic (L, M, I, V); blue, aromatic (W, F. Y); red, basic (R, K, H); light brown, neutral and small (P, G, S, T).